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SEQUENCE LISTING

<110> Li, Jing
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Xiang, Phil
Peng, Yue
Tularik Inc.

<120> PRC17: An Amplified Cancer Gene

<130> 018781-007610US

<140> US 10/071,838

<141> 2001-02-08

<150> US 60/267,615

<151> 2001-02-08

<160> 18

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1650)

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<212> PRT

<213> Homo sapiens

<220>

<223> human PRC17

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Tyr	Leu	Val	Glu	Gly	Glu	Gln	Ala	Leu	Met	Pro	Ile	Thr	Arg	Ile	Ala	290	295	300	
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Trp	Ala	Arg	Phe	Cys	Asn	Arg	Phe	Val	Asp	Thr	Trp	Ala	Arg	Asp	Glu	325	330	335	
Asp	Thr	Val	Leu	Lys	His	Leu	Arg	Ala	Ser	Met	Lys	Lys	Leu	Thr	Arg	340	345	350	
Lys	Gln	Gly	Asp	Leu	Pro	Pro	Pro	Ala	Lys	Pro	Glu	Gln	Gly	Ser	Ser	355	360	365	
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Gly	Asp	Arg	Gln	Ala	Pro	Pro	Gly	Pro	Pro	Ala	Arg	Phe	Pro	Arg	Pro	385	390	395	400
Ile	Trp	Ser	Ala	Ser	Pro	Pro	Arg	Ala	Pro	Arg	Ser	Ser	Thr	Pro	Cys	405	410	415	
Pro	Gly	Gly	Ala	Val	Arg	Glu	Asp	Thr	Tyr	Pro	Val	Gly	Thr	Gln	Gly	420	425	430	
Val	Pro	Ser	Pro	Ala	Leu	Ala	Gln	Gly	Gly	Pro	Gln	Gly	Ser	Trp	Arg	435	440	445	
Phe	Leu	Gln	Trp	Asn	Ser	Met	Pro	Arg	Leu	Pro	Thr	Asp	Leu	Asp	Val	450	455	460	
Glu	Gly	Pro	Trp	Phe	Arg	His	Tyr	Asp	Phe	Arg	Gln	Ser	Cys	Trp	Val	465	470	475	480
Arg	Ala	Ile	Ser	Gln	Glu	Asp	Gln	Leu	Ala	Pro	Cys	Trp	Gln	Ala	Glu	485	490	495	
His	Pro	Ala	Glu	Arg	Val	Arg	Ser	Ala	Phe	Ala	Ala	Pro	Ser	Thr	Asp	500	505	510	
Ser	Asp	Gln	Gly	Thr	Pro	Phe	Arg	Ala	Arg	Asp	Glu	Gln	Pro	Cys	Ala	515	520	525	
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<213> Homo sapiens

<220>
<223> human PRC17 splice variant 1 (exon 3 expanded)

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<220>

<223> human PRC17 splice variant 1 (exon 3 expanded)

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Gly	Pro	Cys	Pro	Pro	Phe	Pro	Val	Pro	Ser	Pro	Gly	Leu	Ser	Pro	Glu	
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Leu	Glu	Arg	Asp	Arg	Ala	Ser	Pro	Phe	Trp	Gly	Ser	Ala	Pro	Arg	Leu	
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Gly	Pro	Leu	Gln	Ala	Pro	Cys	Ser	Ser	Ser	Ala	Leu	Pro	Gly	Leu	Pro	
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		180						185					190			
Lys	Glu	Lys	Gly	Lys	Arg	Ser	Ser	Glu	His	Ile	Gln	Arg	Ile	Asp	Arg	
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Gln	Leu	Leu	Ala	Ser	Glu	Arg	His	Ser	Leu	Gln	Gly	Phe	His	Ser	Pro	
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 Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp Gln
 565 570 575
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 <212> PRT
 <213> Homo sapiens

<220>
 <223> human PRC17 splice variant 2 (exon 10 deleted)

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 50 55 60
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110
 Val Leu Leu Asn Ile Glu Glu Met Lys Leu Lys Asn Pro Gly Arg Tyr
 115 120 125
 Gln Ile Met Lys Glu Lys Gly Lys Arg Ser Ser Glu His Ile Gln Arg
 130 135 140
 Ile Asp Arg Asp Val Ser Gly Thr Leu Arg Lys His Ile Phe Phe Arg
 145 150 155 160
 Asp Arg Tyr Gly Thr Lys Gln Arg Glu Leu Leu His Ile Leu Leu Ala
 165 170 175
 Tyr Glu Glu Tyr Asn Pro Glu Val Gly Tyr Cys Arg Asp Leu Ser His
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 Ala Leu Val Gln Leu Leu Ala Ser Glu Arg His Ser Leu Gln Gly Phe
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 His Ser Pro Asn Gly Gly Thr Val Gln Gly Leu Gln Asp Gln Gln Glu
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 His Val Val Ala Thr Ser Gln Pro Lys Thr Met Gly His Gln Tyr Leu
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 260 265 270
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 275 280 285
 Arg Phe Cys Asn Arg Phe Val Asp Thr Trp Ala Arg Asp Glu Asp Thr
 290 295 300
 Val Leu Lys His Leu Arg Ala Ser Met Lys Lys Leu Thr Arg Lys Gln
 305 310 315 320
 Gly Asp Leu Pro Pro Pro Ala Lys Pro Glu Gln Gly Ser Ser Ala Ser
 325 330 335
 Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly Asp
 340 345 350

Arg Gln Ala Pro Pro Gly Pro Pro Ala Arg Phe Pro Arg Pro Ile Trp
 355 360 365
 Ser Ala Ser Pro Pro Arg Ala Pro Arg Ser Ser Thr Pro Cys Pro Gly
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 Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val Pro
 385 390 395 400
 Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe Leu
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 Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp Ser Asp
 465 470 475 480
 Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Pro Cys Ala Pro Thr
 485 490 495
 Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln Phe Pro
 500 505 510
 Pro Gly Phe
 515

<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:forward primer
 for PCR amplification of PRC17 cDNA

<400> 7
 ggaggggaact gagaactttc ca

22

<210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:reverse primer
 for PCR amplification of PRC17 cDNA

<400> 8
 cgaacagcag tatgtctcca c

21

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
Sequence:fluorescent-labeled PCR TaqMan detection
probe for PRC17

<220>
<221> modified_base
<222> (1)
<223> n = Fam-labeled t

<220>
<221> modified_base
<222> (20)
<223> n = TAMRA-labeled g

<400> 9
ncagggcctt gcctctgcgn 20

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:forward primer
for full-length PRC17 splice variant 1 cDNA
isolation

<400> 10
ggatatggca cggaccca 18

<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:reverse primer
for full-length PRC17 splice variant 1 cDNA
isolation

<400> 11
ggacctggac gtagagggc 19

<210> 12
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR TaqMan
detection probe for PRC17 splice variant 1

<220>
<221> modified_base
<222> (1)
<223> n = Fam-labeled t

<220>
<221> modified_base
<222> (29)
<223> n = TAMRA-labeled a

<400> 12
nctgtctgaa atcataatgg cggaaccan

29

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His epitope
tag

<400> 13
His His His His His His
1 5

<210> 14
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK
epitope tag

<400> 14
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 15
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly-Gly
flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly at positions 6-200 may be present or absent

<400> 15
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 50 55 60
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 65 70 75 80
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 100 105 110
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 115 120 125
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 145 150 155 160
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 165 170 175
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 180 185 190
 Gly Gly Gly Gly Gly Gly Gly Gly Gly
 195 200

<210> 16
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:unique PRC17
 C-terminal peptide

<400> 16
 Pro Ser Thr Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln
 1 5 10 15

Pro Cys

<210> 17
 <211> 786
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human TRE-2/USP6

<400> 17

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Asp	Ile	Leu	Met	Lys	Tyr	Asp	Lys	Gly	His	Arg	Ala	Gly	Leu	Pro	Glu	
			20					25					30			
Asp	Lys	Gly	Pro	Glu	Pro	Val	Gly	Ile	Asn	Ser	Ser	Ile	Asp	Arg	Phe	
		35					40					45				
Gly	Ile	Leu	His	Glu	Thr	Glu	Leu	Pro	Pro	Val	Thr	Ala	Arg	Glu	Ala	
	50					55					60					
Lys	Lys	Ile	Arg	Arg	Glu	Met	Thr	Arg	Thr	Ser	Lys	Trp	Met	Glu	Met	
	65				70					75					80	
Leu	Gly	Glu	Trp	Glu	Thr	Tyr	Lys	His	Ser	Ser	Lys	Leu	Ile	Asp	Arg	
				85					90					95		
Val	Tyr	Lys	Gly	Ile	Pro	Met	Asn	Ile	Arg	Gly	Pro	Val	Trp	Ser	Val	
			100					105					110			
Leu	Leu	Asn	Ile	Gln	Glu	Ile	Lys	Leu	Lys	Asn	Pro	Gly	Arg	Tyr	Gln	
		115					120					125				
Ile	Met	Lys	Glu	Arg	Gly	Lys	Arg	Ser	Ser	Glu	His	Ile	His	His	Ile	
	130					135					140					
Asp	Leu	Asp	Val	Arg	Thr	Thr	Leu	Arg	Asn	His	Val	Phe	Phe	Arg	Asp	
	145				150					155					160	
Arg	Tyr	Gly	Ala	Lys	Gln	Arg	Glu	Leu	Phe	Tyr	Ile	Leu	Leu	Ala	Tyr	
				165					170					175		
Ser	Glu	Tyr	Asn	Pro	Glu	Val	Gly	Tyr	Cys	Arg	Asp	Leu	Ser	His	Ile	
			180					185					190			
Thr	Ala	Leu	Phe	Leu	Leu	Tyr	Leu	Pro	Glu	Glu	Asp	Ala	Phe	Trp	Ala	
		195					200					205				
Leu	Val	Gln	Leu	Leu	Ala	Ser	Glu	Arg	His	Ser	Leu	Pro	Gly	Phe	His	
	210					215					220					
Ser	Pro	Asn	Gly	Gly	Thr	Val	Gln	Gly	Leu	Gln	Asp	Gln	Gln	Glu	His	
	225				230					235					240	
Val	Val	Pro	Lys	Ser	Gln	Pro	Lys	Thr	Met	Trp	His	Gln	Asp	Lys	Glu	
				245					250					255		
Gly	Leu	Cys	Gly	Gln	Cys	Ala	Ser	Leu	Gly	Cys	Leu	Leu	Arg	Asn	Leu	
			260					265					270			
Ile	Asp	Gly	Ile	Ser	Leu	Gly	Leu	Thr	Leu	Arg	Leu	Trp	Asp	Val	Tyr	
		275					280					285				
Leu	Val	Glu	Gly	Glu	Gln	Val	Leu	Met	Pro	Ile	Thr	Ser	Ile	Ala	Leu	
	290					295					300					
Lys	Val	Gln	Gln	Lys	Arg	Leu	Met	Lys	Thr	Ser	Arg	Cys	Gly	Leu	Trp	
	305				310					315					320	

Ala Arg Leu Arg Asn Gln Phe Phe Asp Thr Trp Ala Met Asn Asp Asp
 325 330 335
 Thr Val Leu Lys His Leu Arg Ala Ser Thr Lys Lys Leu Thr Arg Lys
 340 345 350
 Gln Gly Asp Leu Pro Pro Pro Ala Lys Arg Glu Gln Gly Ser Leu Ala
 355 360 365
 Pro Arg Pro Val Pro Ala Ser Arg Gly Gly Lys Thr Leu Cys Lys Gly
 370 375 380
 Tyr Arg Gln Ala Pro Pro Gly Pro Pro Ala Gln Phe Gln Arg Pro Ile
 385 390 395 400
 Cys Ser Ala Ser Pro Pro Trp Ala Ser Arg Phe Ser Thr Pro Cys Pro
 405 410 415
 Gly Gly Ala Val Arg Glu Asp Thr Tyr Pro Val Gly Thr Gln Gly Val
 420 425 430
 Pro Ser Leu Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg Phe
 435 440 445
 Leu Glu Trp Lys Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Ile Gly
 450 455 460
 Gly Pro Trp Phe Pro His Tyr Asp Phe Glu Arg Ser Cys Trp Val Arg
 465 470 475 480
 Ala Ile Ser Gln Glu Asp Gln Leu Ala Thr Cys Trp Gln Ala Glu His
 485 490 495
 Cys Gly Glu Val His Asn Lys Asp Met Ser Trp Pro Glu Glu Met Ser
 500 505 510
 Phe Thr Ala Asn Ser Ser Lys Ile Asp Arg Gln Lys Val Pro Thr Glu
 515 520 525
 Lys Gly Ala Thr Gly Leu Ser Asn Leu Gly Asn Thr Cys Phe Met Asn
 530 535 540
 Ser Ser Ile Gln Cys Val Ser Asn Thr Gln Pro Leu Thr Gln Tyr Phe
 545 550 555 560
 Ile Ser Gly Arg His Leu Tyr Glu Leu Asn Arg Thr Asn Pro Ile Gly
 565 570 575
 Met Lys Gly His Met Ala Lys Cys Tyr Gly Asp Leu Val Gln Glu Leu
 580 585 590
 Trp Ser Gly Thr Gln Lys Ser Val Ala Pro Leu Lys Leu Arg Arg Thr
 595 600 605
 Ile Ala Lys Tyr Ala Pro Lys Phe Asp Gly Phe Gln Gln Gln Asp Ser
 610 615 620
 Gln Glu Leu Leu Ala Phe Leu Leu Asp Gly Leu His Glu Asp Leu Asn
 625 630 635 640

Arg Val His Glu Lys Pro Tyr Val Glu Leu Lys Asp Ser Asp Gly Arg
 645 650 655
 Pro Asp Trp Glu Val Ala Ala Glu Ala Trp Asp Asn His Leu Arg Arg
 660 665 670
 Asn Arg Ser Ile Ile Val Asp Leu Phe His Gly Gln Leu Arg Ser Gln
 675 680 685
 Val Lys Cys Lys Thr Cys Gly His Ile Ser Val Arg Phe Asp Pro Phe
 690 695 700
 Asn Phe Leu Ser Leu Pro Leu Pro Met Asp Ser Tyr Met Asp Leu Glu
 705 710 715 720
 Ile Thr Val Ile Lys Leu Asp Gly Thr Thr Pro Val Arg Tyr Gly Leu
 725 730 735
 Arg Leu Asn Met Asp Glu Lys Tyr Thr Gly Leu Lys Lys Gln Leu Arg
 740 745 750
 Asp Leu Cys Gly Leu Asn Ser Glu Gln Ile Leu Leu Ala Glu Val His
 755 760 765
 Asp Ser Asn Ile Lys Ile Ser Pro Leu His His Leu Gln Met Glu Cys
 770 775 780
 Ser Pro
 785

<210> 18
 <211> 549
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human PRC17.codi

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 Asp Ile Ile Met Lys Tyr Glu Lys Gly His Arg Ala Gly Leu Pro Glu
 20 25 30
 Asp Lys Gly Pro Lys Pro Phe Arg Ser Tyr Asn Asn Asn Val Asp His
 35 40 45
 Leu Gly Ile Val His Glu Thr Glu Leu Pro Pro Leu Thr Ala Arg Glu
 50 55 60
 Ala Lys Gln Ile Arg Arg Glu Ile Ser Arg Lys Ser Lys Trp Val Asp
 65 70 75 80
 Met Leu Gly Asp Trp Glu Lys Tyr Lys Ser Ser Arg Lys Leu Ile Asp
 85 90 95
 Arg Ala Tyr Lys Gly Met Pro Met Asn Ile Arg Gly Pro Met Trp Ser
 100 105 110

Val	Leu	Leu	Asn	Ile	Glu	Glu	Met	Lys	Leu	Lys	Asn	Pro	Gly	Arg	Tyr		
		115					120					125					
Gln	Ile	Met	Lys	Glu	Lys	Gly	Lys	Arg	Ser	Ser	Glu	His	Ile	Gln	Arg		
		130				135					140						
Ile	Asp	Arg	Asp	Ile	Ser	Gly	Thr	Leu	Arg	Lys	His	Met	Phe	Phe	Arg		
	145				150					155					160		
Asp	Arg	Tyr	Gly	Thr	Lys	Gln	Arg	Glu	Leu	Leu	His	Ile	Leu	Leu	Ala		
			165					170						175			
Tyr	Glu	Glu	Tyr	Asn	Pro	Glu	Val	Gly	Tyr	Cys	Arg	Asp	Leu	Ser	His		
		180						185					190				
Ile	Ala	Ala	Leu	Phe	Leu	Leu	Tyr	Leu	Pro	Glu	Glu	Asp	Ala	Phe	Trp		
		195					200					205					
Ala	Leu	Val	Gln	Leu	Leu	Ala	Ser	Glu	Arg	His	Ser	Leu	Gln	Gly	Phe		
	210					215					220						
His	Ser	Pro	Asn	Gly	Gly	Thr	Val	Gln	Gly	Leu	Gln	Asp	Gln	Gln	Glu		
	225			230						235					240		
His	Val	Val	Ala	Thr	Ser	Gln	Ser	Lys	Thr	Met	Gly	His	Gln	Asp	Lys		
			245					250					255				
Lys	Asp	Leu	Cys	Gly	Gln	Cys	Ser	Pro	Leu	Gly	Cys	Leu	Ile	Arg	Ile		
		260					265						270				
Leu	Ile	Asp	Gly	Ile	Ser	Leu	Gly	Leu	Thr	Leu	Arg	Leu	Trp	Asp	Val		
	275						280					285					
Tyr	Leu	Val	Glu	Gly	Glu	Gln	Ala	Leu	Met	Pro	Ile	Thr	Arg	Ile	Ala		
	290					295					300						
Phe	Lys	Val	Gln	Gln	Lys	Arg	Leu	Thr	Lys	Thr	Ser	Arg	Cys	Gly	Pro		
	305				310					315					320		
Trp	Ala	Arg	Phe	Cys	Asn	Arg	Phe	Val	Asp	Thr	Trp	Ala	Arg	Asp	Glu		
			325						330					335			
Asp	Thr	Val	Leu	Lys	His	Leu	Arg	Ala	Ser	Met	Lys	Lys	Leu	Thr	Arg		
		340						345					350				
Lys	Gln	Gly	Asp	Leu	Pro	Pro	Pro	Ala	Lys	Pro	Glu	Gln	Gly	Ser	Ser		
		355					360					365					
Ala	Ser	Arg	Pro	Val	Pro	Ala	Ser	Arg	Gly	Gly	Lys	Thr	Leu	Cys	Lys		
	370					375					380						
Gly	Asp	Arg	Gln	Ala	Pro	Pro	Gly	Pro	Pro	Ala	Arg	Phe	Pro	Arg	Pro		
	385				390					395					400		
Ile	Trp	Ser	Ala	Ser	Pro	Pro	Arg	Ala	Pro	Arg	Ser	Ser	Thr	Pro	Cys		
			405					410					415				
Pro	Gly	Gly	Ala	Val	Arg	Glu	Asp	Thr	Tyr	Pro	Val	Gly	Thr	Gln	Gly		
			420					425					430				

Val Pro Ser Pro Ala Leu Ala Gln Gly Gly Pro Gln Gly Ser Trp Arg
435 440 445

Phe Leu Gln Trp Asn Ser Met Pro Arg Leu Pro Thr Asp Leu Asp Val
450 455 460

Glu Gly Pro Trp Phe Arg His Tyr Asp Phe Arg Gln Ser Cys Trp Val
465 470 475 480

Arg Ala Ile Ser Gln Glu Asp Gln Leu Ala Pro Cys Trp Gln Ala Glu
485 490 495

His Pro Ala Glu Arg Val Arg Ser Ala Phe Ala Ala Pro Ser Thr Asp
500 505 510

Ser Asp Gln Gly Thr Pro Phe Arg Ala Arg Asp Glu Gln Gln Tyr Ala
515 520 525

Pro Thr Ser Gly Pro Cys Leu Cys Gly Leu His Leu Glu Ser Ser Gln
530 535 540

Ala Phe Pro Pro Gly Phe
545